

	Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser	515	520	525	
5	Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe	530	535	540	
	Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln	545	550	555	560
10	Val Gly Pro Gln Val Val Asp Ile Asn Thr Lys Leu Gly Tyr Asn Asn	565	570	575	
15	Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val	580	585	590	
	Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe	595	600	605	
20	Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp	610	615	620	
	Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu	625	630	635	640
25	Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val	645	650	655	
	Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro	660	665	670	
30	Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu	675	680	685	
35	Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala	690	695	700	
	Ile Gln Pro Gly Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly Gln	705	710	715	720
40	Val Val Gly Met Asn Thr Ala Ala Ser	725			
45	<210> SEQ ID NO:10				
	<211> 1797				
	<212> DNA				
	<213> Artificial Sequence				
50	<220> Description of Artificial Sequence:hi-fusion				
	protein TH9-RM15 (designated Mb592)				
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	cat atg cat cac cat cac cac cat atg atg gat ttc ggg ggg tta tta	48			
55	His Met His His His His His His Met Val Asp Phe Gly Ala Leu Pro	1	5	10	15
	ctg gag atc aac tcc ggg ags atg tad gcc ggc cgg gga tgg gcc tgg				36
60	Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser	20	25	30	
	ctg ggg gcc ggg gcc cag atc tgg gac agc atg gcc agt gac ctg ttt				144
	Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe	35	40	45	
65	tgg gcc ggg tgg gcc ttt cag tgg atg gtc tgg agt ctg acg atg ggg				182
	Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly	50	55	60	

	ccg tgg ata ggt tgg tgg ggc ggt cgg atg gta ggg ggc gcc tgg cgg	240
	Ser Trp Ile Gly Ser Met Ala Gly Leu Met Val Ala Ala Ala Ser Pro	48 76 75 80
5	tat ggc cgc tgg atg agc gcc acc ggg ggg cgg gcc gag ctg acc gcc	288
	Tyr Val Ala Trp Met Ser Val Thr Ala Gly Ala Ala Leu Thr Ala	88 96 95
10	gac cag gtc cgg gtc gct ggg ggg gcc taa gag aag ggg tat ggg ctg	336
	Ala Glu Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu	100 105 110
15	acg gtc ccc cgg cgg gta atc gcc gag aac cgt gct gag ctg atg att	384
	Thr Val Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Met Ile	115 120 125
20	ctg aac gcc acc aac atc tgg ggg caa aac acc cgg ggg acc gcc gtc	432
	Leu Ile Ala Thr Asn Leu Leu Gly Glu Asn Thr Pro Ala Ile Ala Val	130 135 140
25	aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc gcc ggg atg	480
	Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Glu Asp Ala Ala Met	145 150 155 160
30	tat ggc tac gcc ggc ggc acc ggg acc ggc acc ggc acc tgg ctg cgg	528
	Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Pro	165 170 175
35	tgc gag gag gcc cgg gag atg acc agc gcc ggt ggt gta ctc gag cgg	576
	Phe Glu Glu His Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Glu	180 185 190
40	gcc gcc ggc gcc gag gag gcc acc gac acc gcc ggg gcc aac cag tgg	624
	Ala Ala Ala Val Glu Glu Ala Ser Asp Thr His Ala Ala Asn Glu Leu	195 200 205
45	atg aac aat gtc ccc cag ggc ctg caa cag ctg gcc cag gcc aag cag	672
	Met Asn Asn Val Pro Glu Ala Leu Glu Glu Leu Ala Glu Pro Thr Glu	210 215 220 225
50	gcc acc acg ccc tat tcc aag ctg ggt ggc ctg tgg aag acc gcc tgg	720
	Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser	225 230 235 240
55	ccg cat cgg tgg cgg atc agc aac atg gta tgg atg gcc aac acc cag	768
	Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His	245 250 255
60	atg tgg atg acc aac tgg ggt gta tgg atg acc aac acc tgg ggc tgg	816
	Met Ser Met Thr Asn Ser Gly Val Ser Ser Thr Asn Thr Leu Ser Ser	260 265 270
65	atg tgg aag gcc ttc gct cgg ggc gcc gcc gcc cag gcc gta caa acc	864
	Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Glu Ala Val Glu Thr	275 280 285 290
70	gac gcc caa aac ggg gtr cgg gcc atg acc tgg ctg ggc agc tgg ctg	912
	Ala Ala Glu Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu	295 300 305 310
75	ggt tct tgg ggt ctg ggc ggt ggg gta gcc gcc aac tgg ggt cgg ggg	960
	Gly Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala	315 320 325 330
80	gcc tgg gtc ggt tgg tgg tgg atg cgg cgg gcc tgg gcc gcc gcc aac	1008
	Ala Ser Val Gly Ser Leu Ser Val Pro Glu Ala Trp Ala Ala Asn	335 340

	cag gca gtc acc cgg ggg ggg cgg ggg ctg cgg ctg acc agc ctg acc	1056
	Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr	
	340 345 350	
5	agg ggc ggc gaa aga ggg ccc ggg cag atg ctg ggc ggg ctg cgg atg	1104
	Ser Ala Ala Gln Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val	
	355 360 365	
10	ggg cag atg ggc gca ags ggc agt ggt ggg ctg agt ggt ggc atg agt	1152
	Gly Gln Met Gln Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg	
	370 375 380	
15	ggt ctg cgg cga ccc tat gtg aag cgg cat tct cgg ggc gcc ggc gat	1200
	Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp	
	385 390 395	
20	acc gcc ctg cgg gcc ttg cgg cag gac cgg ttc gcc gac ttc ccc ggc	1248
	Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala	
	400 405 410 415	
25	ctg ccc ctg gac cgg tcc ggg ctg gtc gcc caa gta ggg ccc cag gta	1296
	Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val	
	420 425 430 435	
30	gta acc atc caa acc aaa ctg ggc taa aac aac gcc gta ggc gcc ggg	1344
	Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly	
	440 445 450 455	
35	acc ggc atc gtc atc gat ccc aac ggt gta gta ctg acc aac aac aac	1392
	Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His	
	460 465 470 475 480	
40	gtg aac ggc ggc gcc acc gac atc aac ggc ttc agc gta ggc tcc ggc	1440
	Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly	
	485 490 495 500 505	
45	caa acc tac ggc gtc gat gta gta ggg tat gac cgc acc cag gat gcc	1488
	Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val	
	505 510 515 520 525	
50	ggc gta ctg cag ctg cgc ggt gcc ggt ggc ctg cgg cgg ggc ggc atc	1536
	Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile	
	530 535 540 545 550	
55	ggt gcc ggc gtc ggc ggt ggt gcc ccc gtc gtc ggc atg ggc aac agc	1584
	Gly Gly Gly Val Ala Val Gly Gln Pro Val Val Ala Met Gly Asn Ser	
	555 560 565 570 575	
60	ggc ggc cag ggc gga aag ccc cgg ggc ggc ccc ggc agc gta gta ggc	1632
	Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala	
	580 585 590 595 600	
65	ctc gcc caa acc gta cag ggc cgg gat cgg ctg acc ggt gcc gaa gag	1680
	Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Gln Gln	
	605 610 615 620 625	
70	acc atg aac ggc ttg atc cag ttc gat gcc ggc atc cag ccc ggt gat	1728
	Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp	
	630 635 640 645 650	
75	tgc ggc ggc ccc gta gta aac ggc caa ggc cag gta gta ggt atc aac	1776
	Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn	
	655 660 665 670 675	
80	acc gcc ggc ccc taggataac	1797
	Thr Ala Ala Ser	
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<210> SEQ ID NO:20
 <211> 596
 <212> PRT
 5 <213> Artificial Sequence
 <220> Description of Artificial Sequence:bi-fusion
 protein Ynm9-Rals (designated Mtb59f)

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 1 5 10 15
 Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
 20 25 30

15 Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
 35 40 45
 Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
 50 55 60

20 Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
 65 70 75 80
 Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
 85 90 95

25 Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
 100 105 110
 Thr Val Pro Pro Pro Val Ile Ala Gln Asn Arg Ala Glu Leu Met Ile
 115 120 125

30 Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
 130 135 140
 35 Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Glu Asp Ala Ala Ala Met
 145 150 155 160
 Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro
 165 170 175

40 Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln
 180 185 190
 45 Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu
 195 200 205
 Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Glu Pro Thr Gln
 210 215 220

50 Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
 225 230 235 240
 Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His
 245 250 255

55 Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
 260 265 270
 60 Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Glu Ala Val Gln Thr
 275 280 285
 Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu
 290 295 300

65 Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala
 305 310 315 320
 Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn

	325	330	335
	Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr		
	340	345	350
5	Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val		
	355	360	365
10	Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg		
	370	375	380
	Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp		
	385	390	395
15	Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala		
	405	410	415
	Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val		
	420	425	430
20	Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly		
	435	440	445
	Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His		
	450	455	460
25	Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly		
	465	470	475
30	Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val		
	485	490	495
	Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile		
	500	505	510
35	Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser		
	515	520	525
40	Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala		
	530	535	540
	Leu Gly Gln Thr Val Tin Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu		
	545	550	555
45	Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp		
	565	570	575
	Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn		
	580	585	590
50	Thr Ala Ala Ser		
	595		

55 (2) INFORMATION FOR SEQ ID NO:21: DPV (MTB.s)

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 500 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

65	GCTGCAGATG TCTTTGACCG TCGGGCGCGG GGTGCTCTCC GCGATCCCG TCGAGCGGTT	60
	CTATTACACC ACTTGCAGTT ACGGGCAGGT AGTACTCTCG CTCAACGCGA CGGATCCGGG	120
	GGCTGCGGCA CAGTTCAAGC TGTATCTGTT GCGGAGTCTC TATTACGSCA APTTCTCTGC	180
	CTACACGCGA CTGACGCGCG CTGCATGTC GCGGCAGTTG CAGGCTGTGC CGGAGGCGCG	240

```

ACAGTACATC GGCCTCTGCG AGTCGGGTGC CGGCTCTGTC AACAACTATT AAGCCCATTC 300
GGGCGCATTC CCGGACCTCC GCATCGTGGC CGGAGCTAGG CGAAATTCGC CGGCTCTGCA 360
AAGGGCTGCA TCCCGGACCC CGGATCTGTC GCGGAGCTCA GCGGAGATTC CCGGCTCTCT 420
CAGAGGCTGC GATCTGTCGC CGAATCTGTC CAGGCTGAGG GATCCATCTG TTCTAGAGCT 480
GGCCGACCTG CTTGAGAGCT

```

(2) INFORMATION FOR SEQ ID NO:22: DFF (MTB.4)

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

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Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
1 5 10 15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
20 25 30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Gln Phe Asn Ala Ser
35 40 45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
25 30 35 40
Gle Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
35 40 45
Gln Tyr Ile Gly Leu Val Gln Ser Val Ala Gly Ser Cys Asn Asn Tyr
45 50 55

```

(2) INFORMATION FOR SEQ ID NO:23: MBL (MTB.8)

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

TGGATTCGCA TAGCGTTTC GCGGCTCGCA CGGAGACCA CGGCGGCGCG GCTCCGGAZ 60
GGGAGCGCGG GACGCTGGGA TTGCGCGGGA CGGCAACCA AGAACCGCGG GTCCGCGCGG 120
TGGGCTGAGC CGGATCGGC GTGATGAGT TGGGAGCG CGCTCGAGTG CGATGCGTGC 180
CGGCGACTCG GAGCGCGGCG AGCAACGAGC CGGAGCGCG CGGAGGATCG GCGAGGCGCG 240
GGGCGGAGCG CTTACCGCAC GACAGCAAT AACGAAATC CGAATCACT GAGCGCGTAC 300
GGGCGGAGCG GAGAGATGTT ATGAGCTTAT TGGAGCTCA TATCGCACG TTGCTGCGAT 360
CCGATTCGCG GTTCGCGCG AGGCGCGCG TGGTGGCGC CACATCGGT CAGGCGCGAG 420
AGCGCGGAT GTTCGCGCG GCTTTTCAG AGGCGCGCG GTTCGCGCGG TTTCGCGCGG 480
CGCATCGCGG GTTTGCGCG CGGCGCGCG AGTCAAGAC CTTGTGGAT GTTCGCGCGG 540
CGAATCGCGG TGGCGCGCG GATACGATAT TGGCGCGCA TGTCT

```

(2) INFORMATION FOR SEQ ID NO:24: MBL (MTB.8)

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1 5 10 15
 Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
 20 25 30
 Gln Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Gln Ser Ser
 35 40 45
 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
 50 55 60
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Gln Ala Lys
 65 70 75 80
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 Phe

(2) INFORMATION FOR SEQ ID NO:25: MTI (MTB9.SA)

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1742 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGGCTCTCTT TCAACGTCAT AAGTTCGGTG GGCACGTGCG CCGCGCGTGC ATATGGGACC 60
 AATAACGGGT GTCCGATGGA TACCTGTAAC GCGCGACGGT AGAGCGGATC AGCGGACGCG 120
 GTCCGAGACA CTACCGGCTC CGCGCTGACG CCGTCCGGCT TCGCGGAGAT CAGGCGCGAG 180
 TTCTCATGGT CGTTAAGGCG TTCCAGACAT GCGAAGGTGC CGCGCGCGCG GACGACGCTGA 240
 GCGAGCTCTG GTCGCGGCGC CGCGCGCGCG GCTGCCACACA CGCGACGATT GAGATGGGAG 300
 CGGATGACCC GTGCGCTGAC ATGCGCGACG GCTCTGATGT ACGGCGGCGC GACGCGCGCT 360
 AGATGCTGCT TGGGCTCGCG GAGGCGGCGG TCGGCGCGCG ACGGCGCGAG CGGCGGCGAG 420
 CGTGAAGCGA GCGATCGCTG CACCGACGAC ACGCGCTGCG CGATCAGGAG CGCTTGGCGC 480
 GTGCGCGAGT CGGCGCGGCG GTCGATGCTG TTGAGGTGAC GGAATGCTG GAGCGCTGCG 540
 TCGTCCGGAG CGCAGACGCT CTGACACGCG AGCGCGTTCG GCTGCTGCGC ACGCGCGCGT 600
 TCGTTCAGCG CGCTTTCGCG ACCGAGAGCG GCGTCAAGAT GCGCGCGCTG CGCGGCTGCT 660
 CGCGCTCTCT CGGCTTCGAG GTCGCGAGCG GCTCGCGCGG CGACTCTTGC AGAGAGCGCT 720
 TCGTGTGATT AATTGGGAGA GAGAGACGAC ATCTGCTTCG TGACACACGA GCGCGAGCGC 780
 CTGCGAGCTG GCGCGCGCGA CTACAGCGGT ATTGCGCGCA CAATGACGCG CCGAGACGCG 840
 GCGCGCGCTG CTCCAAACCG CGGCGGTGCG CCGCGAGCGG CGGATGAGGT ATCGCGCTG 900
 ACCGCGCGCT AGTTTCTCTG GACGCGCGAG ATCTGCGAAA CGTGTGAGCG CCGAGCGCGCG 960
 GCGATTACCG AATGCTTCGT GAGGACGCTG GTGCGCGATT CTGCGCTGCGA CGCGCGCGCG 1020
 GAGCGCGCGA ACCGAGCGCG TGCGCGGTGA AGCGCGCTCG ACGGAGCTGCG TGAGAGAGCG 1080
 GCGGAGACGC CGGAGCTTCT GGTTCAGCGG TCGCGCGCGA GCGCGCGCGA TTGCGGTATC 1140
 GCGGTCTCAT ACGGAGCGCG ATCTAGCGAT TCAATCTAGG GAGGACGCGC AGCGCGCGCT 1200
 CAGTTTCTAT GAGCGATCGG CAGCGGATGC GCGGATGCGG GCGCGCTTTT GAGCGCGCGC 1260
 CCGAGCGCGT GAGGAGCGCG GCGCGCGCGA TGTGCGCGCG CGCGCGAAGC ATTTGCGCGT 1320
 GCGCGCGCGG TCGCATGCGC GAGCGGATCT GCGTGAACGCG CATGACCTAG ATGAGTACGG 1380
 CGTTTTCGCA CATCTGTGAC AGCGTGCACG GGTGCGGTGCG CGGCGTGTGT GCGGAGCGCGA 1440
 ACGAGTACGA ACGGAGCGAG CAGGCTTCTT GCGGAGTCTT GCGGAGTCTT ATGAGTATTA ATTACGCTAT 1500
 CAGAGCGCGG TACGCTTCTT CAGGATGAGA GAGGAGTCTT ATGAGTATTA ATTACGCTAT 1560
 CAGGAGCGCT GAGGCTCATC GCGCGATGAT CCGCGGCTCG CGGCGCTCGC TTGCGCGCGA 1620
 GCGATCGGCT AGGCTGCTGT ATGCTGTTGC CGCGGCTGCG TTGCGCGCGC GCGCGCTGTC 1680
 GGTGCGCTGC CAGGAGTTCG TTACCGGATT GCGCGTACG TTCCAGGTGA TCTGAGAGCA 1740
 G3

(2) INFORMATION FOR SEQ ID NO:26: MTI (MTB9.PA)

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2036 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- 5 (ii) MOLECULES TYPE: DNA (genomic)
(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*
10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTTCATTCCG TTCCGCGGCG CCGCGAAGAC CACCAATCCG GCTGGGGTGG TCGCACACGC 50
GATTGGCTCG GTACAGCTGG GBAATCCGNA TGATTTGGTG TCGATTCGCG TCGATTGCGT 120
GANTTACACG CACGCAAAAG AGCAACGATAT TCGTTTGGCT GATTTGATCG TACTTGGGCA 180
CGCGCATGCG ACCTGTTTCT ACCTCGACCG CACACACAGT GACCTTCGCG CAGAGGCGCA 240
CAACGCGTGG GTTCGCGGGA GCTCTGATAC CACCGCCACA ATTCCGCGCG CTGGTTCGCG 300
GCCCGCGGCT GTTGGCGGCT TTGGCGCGCG CCGAGCGGCT CGGAGATTGG TCGTTTCCCG 360
CAATTTGGCG GTTTCGCGCT CCGGCGCTCG CCGAGAGAGC TTAGCGCGCG ACCGCGATGT 420
CCTTCATGCG CAGAGCGTCC AGCTGCGGTC AGGAGCGGCT GCTTTCAGCG ATACCTCTGG 480
TTCGAGATCG GCGCGGTACA GCGCGCTTTC CTACCTGATA CGGTTTCGCG CACACGCTGA 540
CCTTCGCGCT TCGTTTCGCG GATTTGCTTC CGATTCGCTC TCGCGCGCGC CGGGAATATC 600
TGGAGATGAG GATTCGACCG GCGCTTGGGT AAACGCGGCA CACCGCACGA TCAATTCGCG 660
CGCGGCGGCT TGAATCGAAA TTGACGCTTC CGAGCGGCT TTATCTCGCG CAGAGATTTCA 720
TCCCGTGGCC GTCCTGGTGG CCGTAAATA GCTTGGCTGG CCGGATCTCT CCGGCTGAAAT 780
TGGATGCTCT GACGCGCGCG TCGACGCGCA GTATCTCGAG TGGCGCGCGA ACCCGTTCGA 840
AGCTGTTTAT TGGCGGCTTA CCGACGCTGA ATTTCGCGTG CCAACTGCTG AACATTTGCG 900
AAGCGTGGCG ATCGAATCT ACTTTTTCGCT TTGCGATGAT CTACTCTCTT CCGAGAGAGC 960
GTTCCTGGCA TGAATTCGGA GAGGAGAGCA GCAATGCTGT GGTGACCA CAACCGGAGA 1020
CGTTCGCGCT TCGCGCGCGC AACCTACGCG GTATTGCGCG GCAATTAAG CGCGAGAGAG 1080
CGCGCGCGCG TCGCTCAACG ACCCGAGTAA TCCCGCGAGC CGCGATGAA GTATCAGGCG 1140
TGACCGTGGC TGAATTTGCT GCGCGCGCGC AGATGTAACA AAGGTTTCAG GCGCGAGCGC 1200
CGCGCATTTA CGAAATGTTT GTTACGACGCG TTGTTGGCGA TTTTGGCTCA TACCGAGGCA 1260
CGCGAGCGCG CAGCGCAGCG GCTTCGCGCT GACCGCGGCT GACCGCAACT CCGTAGAGAG 1320
AGCGGAGACA TCGCGAGTTC TCGGTTTCAG GGTTCGCGCG GCGCGCACCG GGTTCAGCTA 1380
TGGCGGTGCA TACACGACGA CGTCTTAGCG ATTCTAGTACT AAGGAGAGAG GCAACATGAT 1440
CTCAGCTTCT ATGACGATC CCGACGCTGT GCGCGGATG GCGCGCGCT TTGAGGTGCA 1500
CGCGCGAGCG GTTGGAGTAC AGGCTTCGCG GATGTTGCGCG TCGCGCGAAA ACATTTCCG 1560
TGGCGGCTGG ATTGGGTTGG CCGAGCGGCG CTGCTAGTAC ACCTGATGCT AGTGAATCA 1620
CGGCTTTTCG AACCTCTGGA ACATCTGCA CCGGCTGCGT GACGCGCTGG TCGCGGAGCT 1680
CAACAACATG GACGAGCGAG AGCGAGCTCT CCGAGCGGCT CTGCGCGACT AGCGCGGAAA 1740
GCGACAGCTG GCGACGCTTT CTGACATTAG GAGAGACGCA ATATGACGAT TAATTACGAG 1800
TTTGGGAGCG TCGACGCTCA TGGCGCGCAT GACCGACGCT AGCGCGGCT GCTTGAAGCG 1860
GAGCATTCAG CCAATGTTGG TGAATGTTGG GCGCGGCTG ACTTTTGGGG GCGGCGCGCT 1920
TGGGTGCTCT GCGAGGATTT CATTAACAAG TGGGCGCGTA ACTTCCAGGT GATCTAGAGCA 1980
CGCGCGACCG CAGCGACGCA GAAGGTCGAG GCTGCGCGCA ACACCATGCG CAGCAACCGAG 2040
AGCGCGCTGG GCTCGAGCTG GCGCTTAAGC TGAATCTGAG TCGCGCGAGC ACACCAACCA 2100
GCGCGTGGCG TCGTGTGCTG TCGCATTAAC TACGACTTGA CCGCTGAGGT AGCGATGAGT 2160
GACGAGATA CCGCGACGCA GATCGCGCTC AACGTCGAGC GCTTCTGGAT GCTTTCAGGG 2220
CTACTGAGAT TCGCTCAAGT TCGCGCTGCG TTACTTTGCT GCGCGTAGCT GCGCATGAT 2280
TGCATGACT GGTTCAGGCA GCGCGCGCGC ATGCGCTGCA TCGCGGAGCA GCGGATTTGT 2340
GTTCAGCGAG GGTTCAGGCA ACAGGTTGCT GCGCGGATGA AGGTTCTTGC CGGCTTGTAT 2400
CTTGAAGTGG TCGCGCTGCT GCGCGCGCGC AAGTTGCTGT AGCGGTTGAT AGCGGAGAG 2460
AACCGCGCTG GCGTTTCGCG TGAATTTGCT GCGCAATGAG TCGCGGCTGT GTTTCGCGCG 2520
CGAGCGCGAG ACTTGGCTTC GCGCGCTGCG GTTTCGAGTG ACATTCAGCT GCGGATGCTG 2580
ACCGGTTTGG ATAGCGCTTC GATCGCGCGC CCGGTAATCG AGGTTTCGGA GCGGATTTCA 2640
CTCGCGGCG CCGCGCGGAG CACCGCGGCT AAGGTTGCGA TGAAGAGAT CTGCTGCGCA 2700
ATTTCGCGAG AGCGAGCGCG CGTTCGCTGT GCGCGAGCGA TCGATTCGCG TCGTTCGCG 2760
CGCGGAGTCC TTGCGGATCT GGTTCGAGCG GCGCGCGCGC CCGGAGAGAG TCGTTCGCG 2820
CGCGGAGTCC TTGCGG 2836

(2) INFORMATION FOR SEQ ID NO:27: NTX (NTX9.9A)

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(iv) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1      5      10      15
Ile Arg Ala Leu Ala Gly Leu Leu Gln Ala Glu His Gln Ala Ile Ile
20      25      30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
35      40      45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
50      55      60
Tyr Gln Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65      70      75      80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
85

```

(2) INFORMATION FOR SEQ ID NO:28: HPCHE1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1290 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

35  CAGGCGTAG CAGAGCGTTC ATCATGATAT CAGACATGAG GGCATTGAC GCGTTGTACG 60
ACCTTCTGCG GATGGGAGTA CCCAACCAAG GGGTATGCTT TACTTGTCTA CTACAGTACT 120
TGGAAAGAGC CATTGAGAGG CTGGTAGCAG CATTTCGCGG GATGAGCTGG TTAGGTTGCG 180
CGCGGAGCAA ATACGCGGCG AAAAACCGCA ACCCGGTGGA TTTTTCGACG GAACTGGGCG 240
ACCTGAGTGC TCACTTCATC AGCTTATATC AAGACACAGC CAACTGAGTC CAGACGAGCC 300
40  AGCACTGCTT GAGAGGCGGC AAGAAAGGTC TGGAGTTGCT GCGCGCGGTG GCTGTGGACC 360
TGACTACATC CCGGTGCTGC GCGCAGCGCC TATCGGCGGC CTTCAGGCG CGTFTTTGCG 420
CGGCGCGGAT GCGCTTATGT GCGCGCGCGC TGGCTTACTT GGTTCGAAAA AGCGTATACA 480
AAGGATCTCA ACTCTTCAA TTGCTTCCCA AATTGCGGAA GTTGGTCGCG GCGGACATG 540
CTGACATCAT TTGGATGTGT GCGGAGTACA TCAAGGCGAC CTTGAGGAGG GTGTGGAGAT 600
45  TGATCAGAAA CCGCTTCAC CCGCTTCAAG AGCTTTGAGG CAACTGCGCG GGTGTGGTGA 660
CGMAGCTGTT GTCTGAGAGG TGGTCAAGAC TGGAGTCTTT CTTTGGCGGC GTCCCGCGCT 720
TGACCGGCGC GACCCAGCGG TTGTGCGAAG TGACTTGGCT GTTGGGTGCG GCGGTTCTGT 780
CGCGCTGCTT GCGCTTGGCT CAGCGGAGTA GCGTTCGAGG CTGAGCTCAC TTGCTCGGCC 840
TCCGCGCATC TCGGCGCGCG TCGGCTTTTG GCGGCTTGGC GAGCTTGAGT CAGGTCGATG 900
50  CGCGCTCAAG TCGGCGGCGG CTACCGGCTC GAGCTTGGTG CCGGCTGCGC CCGCTTGGCT 960
AGCGAGTGGG CGGCGAGTGG CAGCTTGGCT CCGGCGAGG TTCCGAGGTT ATGCGCGGAC 1020
CGTATGAGCT GCGCGGCTGG CAGCGCTTTT CCGGCGGCTC GAAAGGAGAG ACAGCGAAGA 1080
AGTATCTGGA AGGCGCGGCG GCGGCGACTG AAGCGGCGGA GCGGCGCGCA GCGGAGCTG 1140
55  AGCGTGGCTT TCGCAAAAG GTTCTGGTAC GAAAGTCTCT CTAGAGGAGT GCGGAGCGAA 1200

```

(2) INFORMATION FOR SEQ ID NO:29: HPCHE1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

	Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly	
	1 5 10 15	
	Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu	
	20 25 30	
5	Tyr Ser Ser Leu Gln Tyr Phe Gln Lys Ala Leu Gln Gln Leu Ala Ala	
	35 40 45	
	Ala Phe Pro Gly Asp Gly Tyr Leu Gly Ser Ala Ala Asp Lys Tyr Ala	
	50 55 60	
10	Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Gln Leu Ala Asp Leu	
	65 70 75 80	
	Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln	
	85 90 95	
	Thr Thr Arg Asp Ile Leu Gln Gly Ala Lys Lys Gly Leu Gln Phe Val	
	100 105 110	
15	Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala	
	115 120 125	
	Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val	
	130 135 140	
20	Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala	
	145 150 155 160	
	Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Gln Leu Val Ala Ala	
	165 170 175	
	Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr	
	180 185 190	
25	Leu Gly Gln Val Trp Gln Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys	
	195 200 205	
	Gln Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg	
	210 215 220	
30	Gly Trp Ser Asn Leu Gln Ser Phe Phe Ala Gly Val Pro Gly Leu Thr	
	225 230 235 240	
	Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala	
	245 250 255	
	Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser	
	260 265 270	
35	Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Ser Gly Phe	
	275 280 285	
	Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln	
	290 295 300	
40	Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Gln Gln	
	305 310 315 320	
	Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met	
	325 330 335	
	Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser	
	340 345 350	
45	Lys Gly Thr Thr Thr Lys Lys Tyr Ser Gln Gly Ala Ala Ala Gly Thr	
	355 360 365	
	Gln Asp Ala Gln Arg Ala Pro Val Gln Ala Asp Ala Gly Gly Gln	
	370 375 380	
50	Lys Val Leu Val Arg Asn Val Val	
	385 390	

(2) INFORMATION FOR SEQ ID NO:30: MDCW2

55	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1441 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
60	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(iii) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
65	GAGGTTCTCTG GCAATGAGTTT TCGGCTTTT ACCTCGGAA GTGAATTCGA GCGGAATGTA TCGGATTCGC GGCCCGAGGT CGATGCTAC GCGCGCGCC GCTCGRACG GTGTGCGGCG GAGGTTCTCTG TCGGCGCGCG TCGGATTCGC ATCGGTGAGT TCGACGCTGA TCGTTGAGCC GTGATGAGG CCGGCGCGCG CCGGATTCGC GCGCGCGCC ACCCGTAGT TCGGTTACT	60 120 180 240

260 265 270
 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
 275 280 285
 Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
 290 295 300
 Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
 305 310 315
 Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
 320 325 330 335
 10 Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
 340 345 350
 Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
 355 360 365
 15 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Asn Ser Leu Ala Ala Arg
 370 375 380
 Gly Thr Thr Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 385 390 395 400
 Gln Gln Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Gln Gln Pro
 405 410 415
 20 Pro Pro Gly Asn Pro Pro Arg
 420

25 (2) INFORMATION FOR SEQ ID NO:12: ESAT-6

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

35 ATGACGAGAC AGGATGAGAG TTTCGGGGGT ATCGAGGCGG CCGCAGGCGC ATTCGAGGGA
 AATGTCAAGT CCATTCAATC CCTCTTAC GAGGGGAGAC ATCTCTGAC CAGCTCGCA
 GGGGCTGGG GCGGTAGCG TTTCGAGGCG TACT 60 120 154

40 (2) INFORMATION FOR SEQ ID NO:13: ESAT-6

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

50 Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Gln Ala Ala Ala Ser
 1 5 10 15
 Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
 20 25 30
 Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
 35 40 45
 55 Gln Ala Tyr
 50

60 (2) INFORMATION FOR SEQ ID NO:14: T38-1

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGGACGAGAG AAGCGATGCC GGTACCCCTCG CGCAGAGAGC AGGTAAATTC SHSOGATCT 60
 CGGCGGAGCT GAAAGCCGAG ATCGACTAGG TGGAGTCGAC GGCAGGTTCC TTGCAAGGCC 120
 AGTGGCGCGG CGCGCGCGGG ACGGCGCGTC AGGCGCGGCT GGTTCGCTTC CAGAGAGCAG 180
 CGAATAACCA GAAGCAGGGA CTGAGAGAGA TCTCGACGAA TATTCGTCAG GCGGCGCTCC 240
 5 AATCTCGGGA GCGCGACGAG GAGCGAGGAG AGGCGCTGTC CTGCAAGATG GCGTCTGAGC 300
 CGGCTAATAC GAAGGGAAC GAGGCAA 327

(2) INFORMATION FOR SEQ ID NO:35: T538-1

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile 1
 5
 Ser Gly Asp Leu Lys Thr Gln Ile Asn Gln Val Glu Ser Thr Ala Gly 15
 20
 25 Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala 30
 35
 40 Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu 45
 50
 55 Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg 60
 65
 70
 75
 80
 85
 90
 95

(2) INFORMATION FOR SEQ ID NO:36: Tbra2

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 542 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAAATGCGCA CGAGAGGTGA TGGACATCAT CGGAGCCAGC CCGCAACCTC GGAACACGC 60
 GCGACCGGAG CGGCTCCAGC GCGCGCGGGA TACGTCGATC GACATCCGCG TCGCTCGGCT 120
 45 CATTGAGCAG GACATGGGCG TACAGACGCG CGCAGAGATC ACGTACCGCA TCAAGCTGAA 180
 AATTGCTGTT AAGATGAGGC CGGCGCAGCT GCGGAGGAC GCGCGCGGCA GCAAGACGCA 240
 AATGTCAGG GTTCCGGGTT GATTCGTCGG ATTTGTTGTC TGCTCGCGCA GCGCTACGAG 300
 GCGCGGCGCA GTTCCGGGTC CTGCGGTATC CAGGCGTCCA TCGCGATTCC GCGCGCGCAG 360
 CGGAGTTTAA TCTTCGCGCT CGGCGGAG GCGCGGAGTTC GCGCGGAGTTC GCGCGGAGTTC 420
 50 CGGCGGAGTTC CGGCGGAGTTC CGGCGGAGTTC CGGCGGAGTTC CGGCGGAGTTC CGGCGGAGTTC 480
 ACGCTCGGTA GCGCGGCGGTC CTGAGCGGCT CTGAGCGGCT GCGCGGAGTTC GCGCGGAGTTC 540
 542

(2) INFORMATION FOR SEQ ID NO:37: Tbra3

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala 1
 5
 10
 15
 20
 25
 30

	Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile	
	15 40 45	
	Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln	
	50 55 60	
5	Pro Arg	
	65	
10	(2) INFORMATION FOR SEQ ID NO:38: 38 HD	
	(1) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1993 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
20	TGTTTCTGCA CGGCAGCTG GTGAGGAGG GGGCCACCGA ACGCTGTTC TCCTGGCBA 66	
	AGCATGCGGA AACGCGCGA TAGCTCGCG GACTGTGCG GGACGTCAAG GACGCCAAGC 120	
	GCGGAATTG AATGACGAG AAGGTATGG CGTGAATTC GTTTCATA CCGTTTGGC 186	
25	CGTTTGACC GCTGCGCGC TCTGCTAGC ACGGCGGAC TGTGCTGCA AAGCACCGAG 240	
	CGTTGCGCT GAACGCGCG CCGCGCGCG TACTGTGCG ACTACCGCG CGTGTTCGC 306	
	GTGAGCTTG CGGAGACCG GTAGACGCT GCTCTACCG CTGTCACAC TGTGGGTTC 360	
30	GGCTTTCAC GAGAGTATC CGACGCTAC GATCACCGG CAGGCGACG GTTCTGTTTC 420	
	CGGATCGCG CAGGCGCGC CCGGACGCT CAGCTTGGG GCTGCGGAG CTTATCTGTC 480	
35	GGAAGTTGAT ATGCGCGCG AAGAGGCGT GATGACATC GCGCTAGCGA TGTGCGTGA 540	
	GCGGTCAAC TACAACCTTC CCGATTGAG CAGCTACTC AAGCTGAAC GAGAGTCTT 600	
	GGCGGCGAT TACGAGGGA CATTCAAAAC GTTGACATC CCGCATATC CTGCGCTCA 660	
40	CGCGCGCGT AACCTGCGG GCGCGCGGT AGTTGCGGT CACCGCTCG ACGGTGTGG 720	
	TGACACCTTC TTGTTACCG ATGACGCTC CAGCTAGAT CCGGCGGCT GCGGCGATC 780	
45	GGCGGCTTC GGCACACCG TCGCTTCCC GCGGCGCGG GGTGCGCTG GTGAGACCG 840	
	CAGCGCGGC ATGGGACCG GTTGCACCG GACACCGGC TGGTGGGCT ATATCGCAT 900	
	CGCTTCTTC GACCGCGCG GTCAACCGG ACTCGCGAG GCCCAACTG GCAATAGCT 960	
50	TGGCAATTC TTGTTGCGG AAGCGCAAG CATTGAGCG GCGCGGCTG GCTTGGGAT 1020	
	GAAACCGCG CGCAACGAG CATTTCGAT GATCGAGCG CCGGTCGCG ACGGTACAT 1080	
55	GATCATGAG TAGCGTAGC CCAATGCTCA GAAACGCGA AAGGCGCGG CCGCGCGCA 1140	
	GACTTGTAG GATTTCTGC ACTGCGGAT CACGACGCG AACAGGCTT GTTCTCTGA 1200	
60	CGAGTTGAT TTGCGCGCG TCGCGCGCG GTTGTGAGG TTGTTTACG GTTGTATTC 1260	
	GACGTTTTC AGGTAGCTC GTTATGCGC AAGGAGGCG AAGCTCGCT GCGCGATCG 1320	
	GTTGCTTTC GAGCATGCT GCGCGGCTC GTTGAAGTC GCGCGCTCG CCGCGCATC 1380	
65	CGTGTGTCG GTGAGTAGG TGCGGTGAT CCGCTGCTT CCGTGTCTT GTTGTGTGT 1440	
	GTGCTGTGC TCGAGCGAT GGTGCGGAT AGGCTCAGG GTTGTGATTT GTTACCGCG 1500	

ACCGAATGAA ATCCAGGCAA CACCTACGCG GAAACCGTGG TCACGAGGCG GTGGCCGATC 1560
 CGGTGGGCGC CTATACGCG GGGTGGGCGG TGATGTGCG GAGGTGGCG ACCTGGGCAA 1620
 5 TGGCCCGTAT CAGTCGGTGG CCGGTGGTGG TGGAGGCGC GCTGTGATCG GTGGAACGCG 1680
 TGGGAAAGCG GTTGGGCGAG GCTGGGCGAA TAGTCTGGGA ATTGCTGGCG GGAATGCCGA 1740
 10 GGTGGTGGT GGTGTGTG GGGGCAATGA GTTCTGGCGC GTTGTGTGCT CAGCAGATCG 1800
 GTGGGTGGT GCTCAGAC GCTGGCGATG TGGGTGGT GAACTACTTG GCGGCGGACG 1860
 GCGGCAAGCG GAGGCGATG TTAGGTGGCG GTCTGTGTGT GCGGTGTGATG GTGTTGCCA 1920
 15 TTATCGCGAC CAGCAGTAT GAGGTGTGCG GCGAGGTGCG GGTGTGTGCG GCGGAGGTGCG 1980
 GGTGCGGAA TTC 1993

20 (2) INFORMATION FOR SEQ ID NO:39: 38 kD

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
 (B) TYPE: amino acid
 25 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:39:

30 Met Iys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1 5 10 15
 Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
 20 25 30
 35 Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 35 40 45
 Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 40 50 55 60
 Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 65 70 75 80
 45 Ile Thr Ala Glu Gly Thr Gly Ser Gly Ala Gly Ile Ala Glu Ala Ala
 85 90 95
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 100 105 110
 50 Asp Met Ala Ala His Lys Gly Leu Met Asn His Ala Leu Ala Ile Ser
 115 120 125
 Ala Glu Glu Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 130 135 140
 55 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Glu Gly Thr Ile Lys Thr
 145 150 155 160
 60 Trp Asp Asp Pro Glu Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 165 170 175
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190
 65 Phe Leu Phe Thr Glu Tyr Leu Ser Lys Glu Asp Pro Glu Gly Trp Gly
 195 200 205

Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 5 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Glu Ala
 245 250 255
 10 Ser Glu Arg Gly Leu Gly Glu Ala Glu Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Glu Ser Ile Glu Ala Ala Ala Gly Phe
 275 280 285
 15 Ala Ser Lys Thr Pro Ala Asn Glu Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 20 Asn Arg Glu Lys Asp Ala Ala Thr Ala Glu Thr Leu Glu Ala Phe Leu
 325 330 335
 25 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Glu Val
 340 345 350
 His Phe Glu Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 30 Ile Ala Thr Ile Ser Ser
 370

35 (2) INFORMATION FOR SEQ ID NO:40: DPEP

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:40:

45 ATGCAATCACC ATCACCATCA CATGCACTAG GTGGACCCCA ACTTGAGAGC TCGCAAGGGA 60
 CGATTGCTGG CACTGCTGAT CGCGGCGATG GCGAGCGGCA GCTTGTGAC GATTGCGTGT 120
 CTGCTGAGCG CCAACGCGCA TCGGAGGCGA GCGCTGCGCG TACTGAGAGC GCGCGCTCTG 180
 CGCGCTGCGA CCGTCTGAGC GCGGCGGCGA CCGCGGAGAC CTGTGTCTCC CCCGACGCTG 240
 GCGCGCGGCA AGAGCGCGAA TCGCGAGCGG GCGGATCGCA ACACGAGCAT TCGCGCGGCG 300
 50 GCGCGGAGCG CACGCGCGCG ACCGTGTGAT GCGCGAGAG CACCGCAAGC TGTGCGGATC 360
 GACAAACCGG TTGAGGATT CAGCTTGGCG CTGCTGCTG GCTGTGTGGA GTCTGAGCGC 420
 GCGCACTTGG ACTACGCTTC AGCACTGCTC AGCAAAAGCA CTGCGGAGCG GCGCATTTCC 480
 GAGCGCGCGC CCGCGGTTCG CAATGAGAGC GGTGTGCTGC TCGCGCGGCT AGACCAAGAG 540
 55 CTTTAGCGCA GCGCGGAGCG CACCGACTCC AGAGCGCGCG GCGCGTGTGG CTGCGAGCTG 600
 GGTGCTTCT ATATGCGCTA CCGCGCGGCG CCGATCAAGC AGGAAACGCT CTGCTGCGAG 660
 GCGAGCGGCG GTGTGCGAGG CGCGCTGTAT TACGAGTCA AGTTGAGCGA TCGCGCTGAG 720
 CCGATGCGCG AGATCTGAGC GCGCTGAGC GCGTGCAGCG CAGGAGAGCG ACCGAGAGCG 780
 GCGCTGCTGT AGAGCTGCTT TGTGCTGCTG CTCTGAGCG CAGAGAGCG GGTGTGCGAG 840
 60 GCGCGCGCGA AGCGCTGAGC CAATGAGAGC CGCGCTGCG TCGCGCGCGC GCGCGCGCGC 900
 GCGCGCTCT CTGCGAGCGC CGCTGCGCG GCGCGCGCGC CCGCGGAGGT GGTCTGTACG 960
 CCGCGAGAGC GAGACGCGCG GCGGAGCTTA CGCGCTGCG

65 (2) INFORMATION FOR SEQ ID NO:41: DPEP

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

5 Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1 5 10 15
Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20 25 30
10 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35 40 45
Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50 55 60
15 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65 70 75 80
Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85 90 95
Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
100 105 110
20 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
115 120 125
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
130 135 140
25 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
145 150 155 160
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
165 170 175
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
180 185 190
30 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
195 200 205
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
210 215 220
35 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
225 230 235 240
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Asn
245 250 255
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
260 265 270
40 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
275 280 285
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
290 295 300
45 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
305 310 315 320
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
325 330

50 (x) INFORMATION FOR SEQ ID NO:42: TDS4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

60 CGGAGGAGG ATGGTACCC CGGGGATCC CGAGCTGCG ATTGGCCGCG GTTCCGACG 60
CGAGGAAGC CGCTACAGA TGGGCTGCC GAGTAGGCG GATCGCTCG CGATGCGGC 120
GTGACGGCG GCATCAAT TACTGACGGA ACCTTCAGT TTACGACGTA TAATGCTAT 180
AGCACTAGC AGCATATCC GATATGAGC AGTGCAGAC CTGCGCGTG GATCAGCAAG 240
AACTTTGAA TAGGCTCAC GAGGTGGAG CCGCATGCC GAGCTCACG ACTGATGTC 300
65 CCACTACAC GTCCACATC ACGGGGATA AAAAGCGCG CCAACGCTG GATGCTGCG 360
CGGACACAT GCGGACATC GTGCGCGCG GTGCGAAGA GCGCGAGGT CTGCGACCT 420
CGTGCAGCA CGGCGCAGG GGGTATGGG AGTTGATGA GGGGCTGCG AGCGCTGGA 480
ACACGACCG CAGGACACT GTGCGGCGG AATCGCGCG GCGGCTGCG GCGGACATT 540

CGGCGAAGCT AACCGATACG CCGAGGGTGG CCGAGGCCGG TACACCGAAC TCGATGATC 600
 TCAAGGAAGC GCGAAGCAAG CTGGAAGCG GCGACCGAAG CCGATGCGTC GCGATGAGG 660
 GCGATGGGTG GAACACTTNC ACCCTTAGCG TCGAGGCGCA CG 700

5

(i) INFORMATION FOR SEQ ID NO:43: TCR4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:43:

15

Gly Asp Ser Phe Trp Ala Ala Asp Gln Met Ala Arg Gly Phe Val
 1 5 10 15
 Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
 20 25 30 35
 His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
 40 45 50 55
 Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Asn Glu
 60 65 70 75 80
 Ser Gly Leu Ala Arg Met Cys Gly His Asn Pro Glu Asn Ile Phe Phe
 85 90 95 100
 Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
 105 110 115 120
 Ala Thr Glu Gln Arg Thr Asn Arg Asn Gln Ile Leu Ala Ser Gly Val
 125 130 135 140
 Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
 145 150 155 160
 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
 165 170 175 180
 Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
 185 190 195 200
 Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
 205 210 215 220
 Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
 225 230 235 240
 Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
 245 250 255 260
 Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
 265 270 275 280
 Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
 285 290 295 300
 Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
 305 310 315 320
 Leu Pro Gly Phe Asp Gln Gly Gly Gly Leu Arg Pro Asn Lys
 325 330 335 340

40

45

50

55

(i) INFORMATION FOR SEQ ID NO:44: DEPD

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: Genomic DNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:44:

65

ATGAAGCTTA AGTTTGTCTG CTTAGTACT GCGATCTTGG GTTGTCGAC GCGCTCTTGG 60
 TTCTCTACCT CCGTTTCTCG CCGAGATCTA CCGTACCGCG ATCGACCGGA CATGAGAAA 120
 GGTATCTGTC CCGGTACCGC ATGGGTTTT GGTACCTTGG CCGTTCGACA CCGGAGAGAG 180

TACCCGACG OCTCTTTTTC GCACGAGTGG ATSCAAACGK KHTTTACCGG CCGACATHTT 245
 TACTTCGATT GAGTCACCG CGGTGAGGCC TTCCCGGACC CGCGCGCACG GGGTGGTTC 305
 GGTGGGCGAA TTCCTTCGA GCAGCGCAAC CTCCTCTGA 329

5

(2) INFORMATION FOR SEQ ID NO:45: DFFD

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
 1 5 10 15
 20 Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
 25 Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
 30 35 40 45
 25 Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
 50 55 60
 Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
 65 70 75 80
 Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
 85 90 95
 30 Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Gln Gln Pro Asn Ala Pro
 100 105 110

35 <210> SEQ ID NO:46

<211> 92

<212> DNA

<213> Artificial Sequence

<214> Description of Artificial Sequence: tri-fusion
 protein DFF-MFL-MSL (designated Mob3if)

40 <220> (1) .. (900)

cat atg cat cac cat cac cat cac gat ccc gtc gac ggc gtc att aac 18
 5 Met Met His His His His His Asp Pro Val Asp Ala Val Ile Asn 15
 45 acc acc acc aat tac ggg cag gta gta gct ggc ctc aac ggc acc gat 96
 Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp 20 25 30
 50 cgc ggc gcc gcc gca cag ttc aar gcc taa cag gtc ggc cag tcc tat 144
 Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr 35 40 45
 55 tgg cgc aat ttc ctc gcc gca cgg cca cct cag cgc gct gcc atg gcc 192
 Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro His Arg Ala Ala Met Ala 50 55 60
 60 ggc caa tgg caa gct gtc cgc ggg ggc gca cag tac atc ggc att gtc 240
 Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val 65 70 75 80
 65 ggc tgc gtc gcc ggc tcc tgc aac aac tat tgc ctc atc acc att aat 288
 Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Gln Leu Met Thr Ile Asn 85 90 95
 70 tac cag ttc ggc gac gtc gac gct cat ggc gcc atc atc cgc gct cag 336
 Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln 100 105 110

	gag gag tog ntt gag ggg gag cat cag gcc atc gtt cgt gat gag ttg	284
	Ala Ala Ser Leu Glu Ala Glu His Glu Ala Ile Val Arg Asp Val Leu	
	115 120 125	
5	gac ggg ggt gac ttt tgg ggc ggc gcc ggt tog ggg gcc tgc cag gag	412
	Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Glu Glu	
	130 135 140	
10	tac att acc cag atg ggc cgt aac ttc cag gtc atc tac gag gag gcc	460
	Phe Ile Thr Glu Leu Gly Arg Asn Phe Glu Val Ile Tyr Glu Glu Ala	
	145 150 155 160	
15	aac gcc gac ggg cag aag gtc cag gct gcc ggc aac aac atg gcc aac	528
	Asn Ala His Gly Glu Lys Val Glu Ala Ala Gly Asn Asn Met Ala Glu	
	165 170 175	
20	acc gac agc gcc gtc ggc tcc agc tgg gcc aat aat atg agc att ttg	576
	Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu	
	180 185 190	
25	gat gcc cat atc cca cag ttg ggc gcc tcc cag tgg gcc ttt gcc gcc	624
	Asp Ala His Ile Pro Glu Leu Val Ala Ser Glu Ser Ala Phe Ala Ala	
	195 200 205	
30	agc ggc ggg cag atg cgg ccc acc atc ggt cag gcc gag cag gcc ggc	672
	Lys Ala Gly Leu Met Arg His Thr Ile Gly Glu Ala Glu Glu Ala Ala	
	210 215 220	
35	atg tog gcc cag ggc ttt aac cag ggg gag tgg tog gcc gcc ttt cag	720
	Met Ser Ala Glu Ala Phe His Val Gly Glu Ser Ser Ala Ala Phe Glu	
	225 230 235 240	
40	gac gcc cat gcc cgg ttt gtn ggc gcc gcc gcc aac gtc aac acc ttg	768
	Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Leu	
	245 250 255	
45	ttg gat gtc gag cag gcc aat ctg ggt gag gcc gcc ggt acc cat gtc	816
	Leu Asp Val Ala Glu Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val	
	260 265 270	
50	gac gcc gat gcc ggc gcc ggc tog acc tat acc ggg ttc gat acc cat	864
	Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile His	
	275 280 285	
55	acc att gcc ggc cgc tog agc aga tcc ggc tgc taccagagcc cgaagaggag	917
	His Thr Gly Gly Arg Ser Ser Arg Ser Gly Cys	
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60	etga	922
	<215> SEQ ID NO:47	
	<211> 299	
	<212> 388	
	<213> Artificial Sequence	
	<214> Description of Artificial Sequence:tril-fusion	
	protein DFO-MT1-MSL (designated MSL1f)	
60	His Met His His His His His Asp Pro Val Asp Ala Val Ile Asn	
	1 5 10 15	
	Thr Thr Cys Asn Tyr Gly Glu Val Val Ala Ala Leu Asn Ala Thr Asp	
	20 25 30	
65	Pro Gly Ala Ala Ala Glu Phe Asn Ala Ser Pro Val Ala His Ser Tyr	
	35 40 45	

	ttg cgc aat ttc ctg gcc gca cgg cca cct cag cgc gct gcc atg gcc	192
	Leu Arg Asn Phe Leu Ala Ala Pro Pro Glu Arg Ala Ala Met Ala	
	50 55 50	
5	ggc caa ttg caa gct gtg cgg ggg ggg gca cag ttc atc ggc ctt gtc	240
	Ala Glu Leu Glu Ala Val Pro Gly Ala Ala Glu Tyr Ile Gly Leu Val	
	55 70 75	
10	gag tgg gtc gcc ggc tcc tgc aac aac tat gag ctc atg aag att aat	268
	Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn	
	65 80 85	
15	tac cag ttc ggg gac gtc gaa gct cat ggc gcc atg atc cgc gcc cag	336
	Tyr Glu Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Glu	
	105 105 110	
	ggc ggc tgg ctt cag ggc ggc caa cag gcc atc gtc cgt gat tgg ttg	384
	Ala Ala Ser Leu Glu Ala Glu His Glu Ala Ile Val Arg Asp Val Leu	
	115 120 125	
20	gcc gcc ggc gac ctt tgg ggc ggc gcc ggt tgg gtc gct tgc cag gag	432
	Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Glu Glu	
	130 135 140	
25	ttc att acc cag ttg gcc cgt aac ttc cag ttg atc ttc gag cag gcc	480
	Phe Ile Thr Glu Leu Gly Arg Asn Phe Glu Val Ile Tyr Glu Glu Ala	
	145 150 155 160	
30	aac gcc caa ggg cag cag ggc cag gct gcc ggc aac aac atg gag caa	528
	Asn Ala His Gly Glu Lys Val Glu Ala Ala Gly Asn Asn Met Ala Glu	
	165 170 175	
	acc gac agc gcc gtc ggc tcc agc tgg gcc aat agt atg agc ctt ttg	576
	Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu	
	180 185 190	
	gat gcc cat acc cca cag ttg ttg gcc tcc cag tgg ggc ttt gcc gcc	624
	Asp Ala His Ile Pro Glu Leu Val Ala Ser Glu Ser Ala Phe Ala Ala	
	195 200 205	
40	aag gcc ggg ctg atg cgg caa acg atc ggt cag gcc gag cag ggc gcc	672
	Lys Ala Gly Leu Met Arg His Thr Ile Gly His Ala Glu Glu Ala Ala	
	210 215 220	
45	atg tgg gct cag ggc ttt cag cag ggg gag tgg tgg gcc gcc ttt cag	720
	Met Ser Ala Glu Ala Phe His Glu Glu Gly Glu Ser Ser Ala Ala Phe Glu	
	225 230 235 240	
50	gcc gcc cat gcc cgg ctt gtc ggc ggc gcc gcc aaa gtc aac acc ttg	768
	Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Leu	
	245 250 255	
	ttg gat gtc gcc cag ggc aat ttg ggt gag gcc gcc ggt acc tat gtc	816
	Leu Asp Val Ala Glu Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val	
	260 265 270	
	gcc gcc gat gcc ggc gcc ggc tgg acc tat acc ggc ttc gat atc atg	864
	Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Thr Phe Asp Ile Met	
	275 280 285	
60	gat ttc ggg ctt tta cct cgg gaa gtc aat tca agc cga atg tat tcc	912
	Asp Phe Gly Leu Leu Pro Pro His Val Asn Ser Ser Arg Met Tyr Ser	
	290 295 300	
65	ggc ccc ggg cgg gag tgg atg cta gcc gcc gcc gcc gcc gcc ggt	960
	Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp Gly	
	305 310 315 320	

5	gtg gcc gcy gag ctg act tcc gcc gcc gtc tog taa gga tog gtg gtg	1988
	Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val	325 335
10	acg acg ctg atc att gag cag tgg atg ggg cag gcc gcc gcc gcc atg	2056
	Ser Thr Leu Ile Val Glu Pro Tyr Met Gly Pro Ala Ala Ala Met	340 350
15	gcc gcc gcc gcc acg cag tat ctg ggg tog ctg gcc gcc acg gcc gcc	2104
	Ala Ala Ala Ala Thr Pro Tyr Val Gly Tyr Leu Ala Ala Thr Ala Ala	355 365
20	ctg gcc aag gag cag gcc acc cag gcc agt gcc gcc gcc gaa gcc tct	2152
	Leu Ala Ile Glu Thr Ala Thr Glu Ala Arg Ala Ala Glu Ala Phe	370 380
25	ggg aag gcc ttc gcc atg acc gtc cca cca tcc ctc gcc gcc gcc acc	2200
	Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala Asn	385 400
30	acc acc cag ttc atg tog ctg gtc gcc gcc acc att ctg ggg gaa acc	2248
	Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Glu Asn	405 415
35	agt gcc gcc atc gcc gcc acc cag gcc gag tat gcc gaa atg tgg gcc	2296
	Ser Ala Ala Ile Ala Thr Glu Ala Glu Tyr Tyr Ala Glu Met Tyr Ala	420 430
40	caa gcc gct gcc gtc atg tac agc kat gag ggg gaa tct gcc gcc gcc	2344
	Glu Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala Ala	435 445
45	tgg gcc tgg cag cag ttc acc cca ccc gtc cca ggc acc gcc gcc gcc	2392
	Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Glu Gly Thr Gly Pro Ala	450 460
50	ggg ccc gcc gcc gaa gcc ggg ggg acc caa gcc gcc ggt gcc ggg gcc	2440
	Gly Pro Ala Ala Ala Ala Ala Thr Glu Ala Ala Gly Ala Gly Ala	465 480
55	ggt gcc gat gaa cag gcc acc ctg gcc cag ctg ccc cag ggg atc ctg	2488
	Val Ala Asp Ala Glu Ala Thr Leu Ala Glu Leu Pro Pro Gly Ile Leu	485 495
60	agg gcc att ctg tcc gaa ttg gcc gcc acc gct gat cag ctg acc tog	2536
	Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr Ser	500 510
65	gaa ctg ttg ggg atc ggg ctg acc ctc acc cag caa gtc gga tcc gct	2584
	Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Glu Val Gly Ser Ala	515 525
70	acc ctg atc gcc atc ccc acc cgg ata ggg gaa ttg gac gtc atc gcc	2632
	Glu Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile Ala	530 540
75	ctc acc att gaa ccc atc ctg acc gcc acc acc att gcc ctg gcc acc acc	2680
	Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr	545 555
80	acc acc gcc aga ccc tgg tcc atc ggc cta tac ggg acc gcc gcc gcc	2728
	Asn Thr Ala Arg Pro Tyr His Ile Gly Leu Tyr Gly Asn Ala Gly Gly	560 570
85	ctg gga ctg acc cag gcc cat cca ctg agt tog gcc acc gaa gag cag	2776
	Leu Gly Pro Thr Glu Gly His Pro Leu Ser Ser Ala Thr Asp Glu Pro	585 595

	gag cag cac cgg ggc ccc ttc ggg ggc gcg gcg cgg atg tcc ggc ggc 1824 Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Ser Val Ser Ala Gly
5	595 600 605 gic ggc ccc gaa gca tta gtc gga ggg tgg tgg gty cgg ccc agc tgg 1872 Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser Trp
	610 615 620
10	acc acg gcc ggc cgg ggg acc cag ctg gcc gct cag gca ada ccc acc 1920 Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro Thr
	625 630 635 640
15	ttc agc tcc agc gcc ggc ggc gac cgg acg gcc cta acc ggg atg cgg 1968 Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met Pro
	645 650 655
	gaa ggc ctg ctc agc ggg atg gct ttg gcg agc atg gcc gca cgg ggc 2016 Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg Gly
20	660 665 670
	acg acg ggc ggt ggc ggc acc cgt agc ggc acc agc act gac ggc caa 2064 Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly Gln
25	675 680 685
	gag gac gcc cgc aaa ccc cgg gta gct gty att aga gag cag cgg cgg 2112 Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro Pro
	690 695 700
30	ccc ggc aac ccc cgg cgg taagatttct aactaacatc cactgggggc cgtgtgag 2168 Pro Gly Asn Pro Pro Arg 710
35	<210> SEQ ID NO:49 <211> 710 <212> PRT <213> Artificial Sequence <214> Description of Artificial Sequence: beta-tubulin protein DBP-MT1-MBL-MTCC2 (designated MtB715)
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65	

	Phe	Ile	Thr	Glu	Leu	Gly	Arg	Asn	Phe	Glu	Val	Ile	Tyr	Glu	Gln	Ala	
	143					150					155					160	
5	Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala	Gly	Asn	Asn	Met	Ala	Gln	
				165					170						175		
	Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Trp	Ala	Thr	Ser	Met	Ser	Leu	Leu	
				180					185					190			
10	Asp	Ala	His	Ile	Pro	Gln	Leu	Val	Ala	Ser	Gln	Ser	Ala	Phe	Ala	Ala	
				195				200						205			
	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala	Ala	
	210					215					220						
15	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly	Glu	Ser	Ser	Ala	Ala	Phe	Gln	
	225					230				235						240	
	Ala	Ala	His	Ala	Arg	Phe	Val	Ala	Ala	Ala	Lys	Val	Asn	Thr	Leu		
				245					250					255			
20	Leu	Asp	Val	Ala	Gln	Ala	Asn	Leu	Gly	Glu	Ala	Ala	Gly	Thr	Tyr	Val	
				260				265						270			
25	Ala	Ala	Asp	Ala	Ala	Ala	Ala	Ser	Thr	Tyr	Thr	Gly	Phe	Asp	Ile	Met	
			275					280					285				
	Asp	Phe	Gly	Leu	Leu	Pro	Pro	Gln	Val	Asn	Ser	Ser	Arg	Met	Tyr	Ser	
	290					295							300				
30	Gly	Pro	Gly	Pro	Glu	Ser	Met	Leu	Ala	Ala	Ala	Ala	Ala	Trp	Asp	Gly	
	305					310					315				320		
	Val	Ala	Ala	Glu	Leu	Thr	Met	Ala	Ala	Val	Met	Tyr	Gly	Ser	Val	Val	
				325						330					335		
35	Ser	Thr	Leu	Ile	Val	Glu	Pro	Trp	Met	Gly	Pro	Ala	Ala	Ala	Ala	Met	
			340					345							350		
40	Ala	Ala	Ala	Ala	Thr	Pro	Tyr	Val	Gly	Trp	Leu	Ala	Ala	Thr	Ala	Ala	
				355				360						365			
	Leu	Ala	Lys	Glu	Thr	Ala	Thr	Gln	Ala	Arg	Ala	Ala	Ala	Glu	Ala	Phe	
			370				375						380				
45	Gly	Thr	Ala	Phe	Ala	Met	Thr	Val	Pro	Pro	Ser	Leu	Val	Ala	Ala	Asn	
			385			390					395					400	
	Arg	Ser	Arg	Leu	Met	Ser	Leu	Val	Ala	Ala	Asn	Ile	Leu	Gly	Gln	Asn	
			405					410							415		
50	Ser	Ala	Ala	Ile	Ala	Ala	Thr	Gln	Ala	Glu	Tyr	Ala	Glu	Met	Trp	Ala	
			420					425						430			
55	Gln	Asp	Ala	Ala	Val	Met	Tyr	Ser	Tyr	Gln	Gly	Ala	Ser	Ala	Ala	Ala	
			435					440					445				
	Ser	Ala	Leu	Pro	Pro	Phe	Thr	Pro	Pro	Val	Gln	Gly	Thr	Gly	Pro	Ala	
			450				455						460				
60	Gly	Pro	Ala	Ala	Ala	Ala	Ala	Thr	Gln	Ala	Ala	Gly	Ala	Gly	Ala	Ala	
			465				470				475					480	
	Val	Ala	Asp	Ala	Gln	Ala	Thr	Leu	Ala	Gln	Leu	Pro	Pro	Gly	Ile	Leu	
			485					490							495		
65	Ser	Asp	Ile	Leu	Ser	Ala	Leu	Ala	Ala	Asn	Ala	Asp	Pro	Leu	Thr	Ser	
			500					505						510			

	Gly	Leu	Leu	Gly	Ile	Ala	Ser	Thr	Leu	Asn	Pro	Gln	Val	Gly	Ser	Ala	
	518							520					525				
5	Gln	Pro	Ile	Val	Ile	Pro	Thr	Pro	Ile	Gly	Gln	Leu	Asp	Val	Ile	Ala	
	530					535						540					
	Leu	Tyr	Ile	Ala	Ser	Ile	Ala	Thr	Gly	Ser	Ile	Ala	Leu	Ala	Ile	Thr	
	545				550					555					560		
10	Asn	Thr	Ala	Arg	Pro	Trp	His	Ile	Gly	Leu	Tyr	Gly	Asn	Ala	Gly	Gly	
					565				570						575		
	Leu	Gly	Pro	Thr	Gln	Gly	His	Pro	Leu	Ser	Ser	Ala	Thr	Asp	Gln	Pro	
15					580				585					590			
	Glu	Pro	His	Trp	Gly	Pro	Phe	Gly	Gly	Ala	Ala	Pro	Val	Ser	Ala	Gly	
		595				600							605				
	Val	Gly	His	Ala	Ala	Leu	Val	Gly	Ala	Leu	Ser	Val	Pro	His	Ser	Trp	
20		610					615					620					
	Thr	Thr	Ala	Ala	Pro	Glu	Ile	Gln	Leu	Ala	Val	Gln	Ala	Thr	Pro	Thr	
		625				630				635						640	
25	Phe	Ser	Ser	Ser	Ala	Gly	Ala	Asp	Pro	Thr	Ala	Leu	Asn	Gly	Met	Pro	
					645				650						655		
	Ala	Gly	Leu	Leu	Ser	Gly	Met	Ala	Leu	Ala	Ser	Leu	Ala	Ala	Arg	Gly	
			660				665							670			
30	Thr	Thr	Gly	Gly	Gly	Gly	Thr	Arg	Ser	Gly	Thr	Ser	Thr	Asp	Gly	Gln	
			675					680						685			
	Gln	Asp	Gly	Arg	Lys	Pro	Pro	Val	Val	Val	Ile	Arg	Gln	Gln	Pro	Pro	
35		690				695						700					
	Pro	Gly	Asn	Pro	Pro	Arg											
		705				710											
40																	